

OIKE

RAW SEQUENCE LISTING

DATE: 07/20/2001

PATENT APPLICATION: US/09/894,749

TIME: 11:25:14

Input Set : N:\Crf3\RULE60\09894749.txt

Output Set: N:\CRF3\07202001\I894749.raw

5 <110> APPLICANT: Hodge, Martin R.
7 Yowe, David
11 <120> TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
15 <130> FILE REFERENCE: 5800-19, 035800/174680
19 <140> CURRENT APPLICATION NUMBER: 09/894,749
21 <141> CURRENT FILING DATE: 2001-06-27
23 <150> PRIOR APPLICATION NUMBER: 09/244,314
25 <151> PRIOR FILING DATE: 1999-02-04
27 <160> NUMBER OF SEQ ID NOS: 4
31 <170> SOFTWARE: PatentIn Ver. 2.0
35 <210> SEQ ID NO: 1
37 <211> LENGTH: 2217
39 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
45 <220> FEATURE:
47 <221> NAME/KEY: CDS
49 <222> LOCATION: (160)..(867)
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63 gatgtaataa attagacatc tcttcatttt agagagaag atg gaa aca aca ttg 174
65 Met Glu Thr Thr Leu
67 1 5
71 ctt ttc ttt tct caa ata aat atg tgt gaa tca aaa gaa aaa act ttt 222
73 Leu Phe Phe Ser Gln Ile Asn Met Cys Glu Ser Lys Glu Lys Thr Phe
75 10 15 20
79 ttc aag tta ata cat ggt tca gga aaa gaa gaa aca agc aaa gaa gcc 270
81 Phe Lys Leu Ile His Gly Ser Gly Lys Glu Glu Thr Ser Lys Glu Ala
83 25 30 35
87 aaa atc aga gct aag gaa aaa aga aat aga cta agt ctt ctt gtg cag 318
89 Lys Ile Arg Ala Lys Glu Lys Arg Asn Arg Leu Ser Leu Leu Val Gln
91 40 45 50
95 aaa cct gag ttt cat gaa gac acc cgc tcc agt aga tct ggg cac ttg 366
97 Lys Pro Glu Phe His Glu Asp Thr Arg Ser Ser Arg Ser Gly His Leu
99 55 60 65
103 gcc aaa gaa aca aga gtc tcc cct gaa gag gca gtg aaa tgg ggt gaa 414
105 Ala Lys Glu Thr Arg Val Ser Pro Glu Glu Ala Val Lys Trp Gly Glu
107 70 75 80 85
111 tca ttt gac aaa ctg ctt tcc cat aga gat gga cta gag gct ttt acc 462
113 Ser Phe Asp Lys Leu Leu Ser His Arg Asp Gly Leu Glu Ala Phe Thr
115 90 95 100
119 aga ttt ctt aaa act gaa ttc agt gaa gaa aat att gaa ttt tgg ata 510
121 Arg Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn Ile Glu Phe Trp Ile
123 105 110 115
127 gcc tgt gaa gat ttc aag aaa agc aag gga cct caa caa att cac ctt 558
129 Ala Cys Glu Asp Phe Lys Lys Ser Lys Gly Pro Gln Gln Ile His Leu
131 120 125 130

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135 aaa gca aaa gca ata tat gag aaa ttt ata cag act gat gcc cca aaa 606
137 Lys Ala Lys Ala Ile Tyr Glu Lys Phe Ile Gln Thr Asp Ala Pro Lys
139 135 140 145
143 gag gtt aac ctt gat ttt cac aca aaa gaa gtc att aca aac agc atc 654
145 Glu Val Asn Leu Asp Phe His Thr Lys Glu Val Ile Thr Asn Ser Ile
147 150 155 160 165
151 act caa cct acc ctc cac agt ttt gat gct gca caa agc aga gtg tat 702
153 Thr Gln Pro Thr Leu His Ser Phe Asp Ala Ala Gln Ser Arg Val Tyr
155 170 175 180
159 cag ctc atg gaa caa gac agt tat aca cgt ttt ctg aaa tct gac atc 750
161 Gln Leu Met Glu Gln Asp Ser Tyr Thr Arg Phe Leu Lys Ser Asp Ile
163 185 190 195
167 tat tta gac ttg atg gaa gga aga cct cag aga cca aca aat ctt agg 798
169 Tyr Leu Asp Leu Met Glu Gly Arg Pro Gln Arg Pro Thr Asn Leu Arg
171 200 205 210
175 aga cga tca cgc tca ttt acc tgc aat gaa ttc caa gat gta caa tca 846
177 Arg Arg Ser Arg Ser Phe Thr Cys Asn Glu Phe Gln Asp Val Gln Ser
179 215 220 225
183 gat gtt gcc att tgg tta taa agaaaattga ttttgctcat ttttatgaca 897
185 Asp Val Ala Ile Trp Leu
187 230 235
191 aacttataca tctgcttcta acatatcgca tgtttatggt aagatttggt cccatccctt 957
195 aaactgaaat atgtcatgtg aaattatttt aaaaatgtaa aaacaaaact ttctgctaac 1017
199 aaaatacata cagtatctgc cagtatatctc tgtaaaacct tctatttgat gtcattccat 1077
203 ttataatcag aaaaaaaact tatttcttaa tcaaaaaggca gtacaaaaaa agtaataatg 1137
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255 ttcttgtaa gcaaatctcc ttaagtaatt attattcaaa taagattata ctcatatc 1917
259 tatatgtcac tgttttaaa agatatttaa tttttaatgt gtgttacatg gtctgtaa 1977
263 atttgatatt aaaaatgcc tgcattaggc tttggaaatt taatgttagt tgaaatgtaa 2037
267 aatgtgaaaa ctttagatca tttgtagtaa taaatatttt taacttcatt catacagtta 2097
271 agtttatctg acaataaaag ctctgactga atgttgatta tccttcctat tatgtaataa 2157
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283 <211> LENGTH: 235
285 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
291 <400> SEQUENCE: 2
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299 Lys Glu Lys Thr Phe Phe Lys Leu Ile His Gly Ser Gly Lys Glu Glu
301              20              25              30
305 Thr Ser Lys Glu Ala Lys Ile Arg Ala Lys Glu Lys Arg Asn Arg Leu
307              35              40              45
311 Ser Leu Leu Val Gln Lys Pro Glu Phe His Glu Asp Thr Arg Ser Ser
313              50              55              60
317 Arg Ser Gly His Leu Ala Lys Glu Thr Arg Val Ser Pro Glu Glu Ala
319 65              70              75              80
323 Val Lys Trp Gly Glu Ser Phe Asp Lys Leu Leu Ser His Arg Asp Gly
325              85              90              95
329 Leu Glu Ala Phe Thr Arg Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn
331              100             105             110
335 Ile Glu Phe Trp Ile Ala Cys Glu Asp Phe Lys Lys Ser Lys Gly Pro
337              115             120             125
341 Gln Gln Ile His Leu Lys Ala Lys Ala Ile Tyr Glu Lys Phe Ile Gln
343              130             135             140
347 Thr Asp Ala Pro Lys Glu Val Asn Leu Asp Phe His Thr Lys Glu Val
349 145             150             155             160
353 Ile Thr Asn Ser Ile Thr Gln Pro Thr Leu His Ser Phe Asp Ala Ala
355             165             170             175
359 Gln Ser Arg Val Tyr Gln Leu Met Glu Gln Asp Ser Tyr Thr Arg Phe
361             180             185             190
365 Leu Lys Ser Asp Ile Tyr Leu Asp Leu Met Glu Gly Arg Pro Gln Arg
367             195             200             205
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391 <213> ORGANISM: Mus sp.
395 <220> FEATURE:
397 <221> NAME/KEY: CDS
399 <222> LOCATION: (134)..(841)
403 <400> SEQUENCE: 3
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413 actgggacag aat atg gat atg tca ctg gtt ttc ttc tct caa tta aat 169
415             Met Asp Met Ser Leu Val Phe Phe Ser Gln Leu Asn
417              1              5              10
421 atg tgt gaa tca aaa gag aaa act ttt ttc aaa cta atg cat ggg tca 217
423 Met Cys Glu Ser Lys Glu Lys Thr Phe Phe Lys Leu Met His Gly Ser
425             15             20             25
429 ggg aaa gaa gaa aca agc atc gag gcc aaa atc aga gcg aaa gaa aaa 265
431 Gly Lys Glu Glu Thr Ser Ile Glu Ala Lys Ile Arg Ala Lys Glu Lys
433             30             35             40
437 agg aat aga cta agt ctt ctc cta cag agg cct gac ttc cat gga gag 313

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439 Arg Asn Arg Leu Ser Leu Leu Leu Gln Arg Pro Asp Phe His Gly Glu
441 45 50 55 60
445 act caa gcc agt aga tct gcc ctc ttg gcc aaa gaa aca aga gtc tct 361
447 Thr Gln Ala Ser Arg Ser Ala Leu Leu Ala Lys Glu Thr Arg Val Ser
449 65 70 75
453 cct gaa gaa gca gtg aaa tgg gct gaa tca ttt gac aaa ttg ctc tct 409
455 Pro Glu Glu Ala Val Lys Trp Ala Glu Ser Phe Asp Lys Leu Leu Ser
457 80 85 90
461 cat aga gat gga gtg gat gct ttt acc aga ttt ctt aaa act gaa ttc 457
463 His Arg Asp Gly Val Asp Ala Phe Thr Arg Phe Leu Lys Thr Glu Phe
465 95 100 105
469 agt gag gag aac att gaa ttt tgg gtc gcc tgt gaa gac ttc aag aaa 505
471 Ser Glu Glu Asn Ile Glu Phe Trp Val Ala Cys Glu Asp Phe Lys Lys
473 110 115 120
477 tgc aag gaa cct caa caa atc atc cta aaa gca aag gca atc tat gag 553
479 Cys Lys Glu Pro Gln Gln Ile Ile Leu Lys Ala Lys Ala Ile Tyr Glu
481 125 130 135 140
485 aaa ttc att cag aat gat gcc ccc aaa gag gtt aac att gat ttt cat 601
487 Lys Phe Ile Gln Asn Asp Ala Pro Lys Glu Val Asn Ile Asp Phe His
489 145 150 155
493 act aaa gaa gta att gct aag agc atc gcc cag ccc act ctc cac agt 649
495 Thr Lys Glu Val Ile Ala Lys Ser Ile Ala Gln Pro Thr Leu His Ser
497 160 165 170
501 ttt gat acg gca caa agc aga gtg tac cag ctc atg gaa cat gac agt 697
503 Phe Asp Thr Ala Gln Ser Arg Val Tyr Gln Leu Met Glu His Asp Ser
505 175 180 185
509 tat aaa cgc ttt ttg aaa tct gag acc tac tta cat ttg ata gaa gga 745
511 Tyr Lys Arg Phe Leu Lys Ser Glu Thr Tyr Leu His Leu Ile Glu Gly
513 190 195 200
517 aga cct cag aga cca aca aac ctt agg aga cga tca cga tca ttt act 793
519 Arg Pro Gln Arg Pro Thr Asn Leu Arg Arg Arg Ser Arg Ser Phe Thr
521 205 210 215 220
525 tac aat gat ttc caa gat gta aag tca gat gtt gcc att tgg tta tga 841
527 Tyr Asn Asp Phe Gln Asp Val Lys Ser Asp Val Ala Ile Trp Leu
529 225 230 235
533 gtaaaagtca tttgtcttct tttgatagtg tatgtgtata tctaaaatat atactaatac 901
537 taatgtgtac ttctaaaata tagcttgtgt ataagaagag atgatttcat ttttaaaata 961
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559 <210> SEQ ID NO: 4
561 <211> LENGTH: 235
563 <212> TYPE: PRT
565 <213> ORGANISM: Mus sp.
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577 Lys Glu Lys Thr Phe Phe Lys Leu Met His Gly Ser Gly Lys Glu Glu

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591          50          55          60
595 Arg Ser Ala Leu Leu Ala Lys Glu Thr Arg Val Ser Pro Glu Glu Ala
597          65          70          75          80
601 Val Lys Trp Ala Glu Ser Phe Asp Lys Leu Leu Ser His Arg Asp Gly
603          85          90          95
607 Val Asp Ala Phe Thr Arg Phe Leu Lys Thr Glu Ser Gln Glu Asn
609          100          105          110
613 Ile Glu Phe Trp Val Ala Cys Glu Asp Phe Lys Lys Cys Lys Glu Pro
615          115          120          125
619 Gln Gln Ile Ile Leu Lys Ala Lys Ala Ile Tyr Glu Lys Phe Ile Gln
621          130          135          140
625 Asn Asp Ala Pro Lys Glu Val Asn Ile Asp Phe His Thr Lys Glu Val
627          145          150          155          160
631 Ile Ala Lys Ser Ile Ala Gln Pro Thr Leu His Ser Phe Asp Thr Ala
633          165          170          175
637 Gln Ser Arg Val Tyr Gln Leu Met Glu His Asp Ser Tyr Lys Arg Phe
639          180          185          190
643 Leu Lys Ser Glu Thr Tyr Leu His Leu Ile Glu Gly Arg Pro Gln Arg
645          195          200          205
649 Pro Thr Asn Leu Arg Arg Arg Ser Arg Ser Phe Thr Tyr Asn Asp Phe
651          210          215          220
655 Gln Asp Val Lys Ser Asp Val Ala Ile Trp Leu
657 225          230          235

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VERIFICATION SUMMARY

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